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## RAW SEQUENCE LISTING

DATE: 07/30/2001

PATENT APPLICATION: US/09/880,708

TIME: 12:12:03

Input Set : N:\Cr3\RULE60\09880708.txt

Output Set: N:\CRF3\07302001\I880708.raw

## SEQUENCE LISTING

## C--&gt; 6 (1) GENERAL INFORMATION:

8 (i) APPLICANT: Lee, Se-Jin  
9 Huynh, Thanh

## C--&gt; 11 (ii) TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5

13 (iii) NUMBER OF SEQUENCES: 28

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Gray Cary Ware &amp; Freidenrich LLP

17 (B) STREET: 4365 Executive Drive, Suite 1600

18 (C) CITY: San Diego

19 (D) STATE: CA

20 (E) COUNTRY: USA

21 (F) ZIP: 92121-2189

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Diskette

26 (B) COMPUTER: IBM Compatible

27 (C) OPERATING SYSTEM: Windows95

28 (D) SOFTWARE: FastSEQ for Windows Version 2.0

30 (vi) CURRENT APPLICATION DATA:

C--&gt; 31 (A) APPLICATION NUMBER: US/09/880,708

C--&gt; 32 (B) FILING DATE: 12-Jun-2001

38 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 09/145,060

36 (B) FILING DATE:

39 (A) APPLICATION NUMBER: 08/003,144

40 (B) FILING DATE: 12-JAN-1993

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Lisa A. Haile, Ph.D.

44 (B) REGISTRATION NUMBER: 38,347

45 (C) REFERENCE/DOCKET NUMBER: 07265/057002

47 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: 858/677-1456

49 (B) TELEFAX: 619/677-1465

52 (2) INFORMATION FOR SEQ ID NO: 1:

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 28 base pairs

56 (B) TYPE: nucleic acid

57 (C) STRANDEDNESS: single

58 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: Genomic DNA

62 (vii) IMMEDIATE SOURCE:

63 (B) CLONE: 136

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

68 CCGGAATTCTG GNTGGGARMG NTGGRTNR

28

71 (2) INFORMATION FOR SEQ ID NO: 2:

72 (i) SEQUENCE CHARACTERISTICS:

73 (A) LENGTH: 42 base pairs

ENTERED

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74         (B) TYPE: nucleic acid
75         (C) STRANDEDNESS: single
76         (D) TOPOLOGY: linear
78         (ii) MOLECULE TYPE: Genomic DNA
80         (vii) IMMEDIATE SOURCE:
81             (B) CLONE: 121
83         (ix) FEATURE:
84             (A) NAME/KEY: Coding Sequence
85             (B) LOCATION: 1..42
C--> 86         (D) OTHER INFORMATION: / N at residue 13, 25 and 28 = Inosine
88         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
90 CCGGAATTCTC CANCCRCAYT CRTCNACNAC CATRTCYTCR TA 42
93 (2) INFORMATION FOR SEQ ID NO: 3:
95     (i) SEQUENCE CHARACTERISTICS:
96         (A) LENGTH: 7 amino acids
97         (B) TYPE: amino acid
98         (D) TOPOLOGY: linear
100     (ii) MOLECULE TYPE: peptide
102     (vii) IMMEDIATE SOURCE:
103         (B) CLONE: 136
105     (ix) FEATURE:
106         (B) LOCATION: 1..7
C--> 107         (D) OTHER INFORMATION: Xaa at residue 4 = Arg or Ser;
C--> 108 Xaa at residue 6 and 7 = Val, Ile or Met
110     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
W--> 112 Gly Trp Glu Xaa Trp Xaa Xaa
113     1             5
116 (2) INFORMATION FOR SEQ ID NO: 4:
118     (i) SEQUENCE CHARACTERISTICS:
119         (A) LENGTH: 11 amino acids
120         (B) TYPE: amino acid
121         (D) TOPOLOGY: linear
123     (ii) MOLECULE TYPE: peptide
125     (vii) IMMEDIATE SOURCE:
126         (B) CLONE: 121
128     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
130 Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys
131     1             5             10
134 (2) INFORMATION FOR SEQ ID NO: 5:
136     (i) SEQUENCE CHARACTERISTICS:
137         (A) LENGTH: 35 base pairs
138         (B) TYPE: nucleic acid
139         (C) STRANDEDNESS: single
140         (D) TOPOLOGY: linear
142     (ii) MOLECULE TYPE: Genomic DNA
144     (vii) IMMEDIATE SOURCE:
145         (B) CLONE: 141
147     (ix) FEATURE:
148         (A) NAME/KEY: Coding Sequence

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Input Set : N:\Crf3\RULE60\09880708.txt

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149          (B) LOCATION: 1..35
C--> 150      (D) OTHER INFORMATION: N at residue 12, 27, 30 and 33 = Inosine
152          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
154 CCGGAATTCG GNTGGVANRA YTGGRNRTN KCNCC 35
157 (2) INFORMATION FOR SEQ ID NO: 6:
159     (i) SEQUENCE CHARACTERISTICS:
160         (A) LENGTH: 33 base pairs
161         (B) TYPE: nucleic acid
162         (C) STRANDEDNESS: single
163         (D) TOPOLOGY: linear
165     (ii) MOLECULE TYPE: Genomic DNA
167     (vii) IMMEDIATE SOURCE:
168         (B) CLONE: 145
170     (ix) FEATURE:
171         (A) NAME/KEY: Coding Sequence
172         (B) LOCATION: 1..33
C--> 173      (D) OTHER INFORMATION: N at residue 13, 19, 25 and 28 = Inosine
176          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
178 CCGGAATTCR CANSRCRANG MNTCNACNRY CAT 33
181 (2) INFORMATION FOR SEQ ID NO: 7:
183     (i) SEQUENCE CHARACTERISTICS:
184         (A) LENGTH: 9 amino acids
185         (B) TYPE: amino acid
186         (D) TOPOLOGY: linear
188     (ii) MOLECULE TYPE: peptide
190     (vii) IMMEDIATE SOURCE:
191         (B) CLONE: 141
193     (ix) FEATURE:
194         (B) LOCATION: 1..9
C--> 195      (D) OTHER INFORMATION: Xaa at residue 3 = His, Gln, Asn,
C--> 196 Lys, Glu or Asp; Xaa at residue 4 = Asp or Asn; Xaa
C--> 197 at residues 6 and 7 = Val, Ile or Met; Xaa at
C--> 198 residue 8 = Glu or Ser
201          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
W--> 203 Gly Trp Xaa Xaa Trp Xaa Xaa Xaa Pro
204      1      5
207 (2) INFORMATION FOR SEQ ID NO: 8:
209     (i) SEQUENCE CHARACTERISTICS:
210         (A) LENGTH: 8 amino acids
211         (B) TYPE: amino acid
212         (D) TOPOLOGY: linear
214     (ii) MOLECULE TYPE: peptide
216     (vii) IMMEDIATE SOURCE:
217         (B) CLONE: 145
219     (ix) FEATURE:
220         (B) LOCATION: 1..8
C--> 221      (D) OTHER INFORMATION: Xaa at residues 2 and 3 = Val, Ile,
C--> 222 Met, Thr or Ala; Xaa at residue 4 = Asp or Glu; Xaa
C--> 223 at residue 5 = Ala or Ser; Xaa at residue 7 = Gly,

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/880,708

DATE: 07/30/2001

TIME: 12:12:03

Input Set : N:\Crif3\RULE60\09880708.txt

Output Set: N:\CRF3\07302001\I880708.raw

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C--> 224 Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile, Leu,
C--> 225 Lys, Met, Phe Pro, Ser, Thr, Trp, Tyr, and Val.
227 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
W--> 229 Met Xaa Xaa Xaa Xaa Cys Xaa Cys
230 1 5
232 (2) INFORMATION FOR SEQ ID NO: 9:
234 (i) SEQUENCE CHARACTERISTICS:
235 (A) LENGTH: 2329 base pairs
236 (B) TYPE: nucleic acid
237 (C) STRANDEDNESS: single
238 (D) TOPOLOGY: linear
240 (ii) MOLECULE TYPE: Genomic DNA
242 (vii) IMMEDIATE SOURCE:
243 (B) CLONE: GD-5
245 (ix) FEATURE:
246 (A) NAME/KEY: Coding Sequence
247 (B) LOCATION: 322...1806
249 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
251 TTCAAGCCCT CAGTCAGTTG TGC GGGAGAA AGGGGGCGGT CGGCTTTCTC CTTTCAAGAA 60
252 CGAGTTATTT TCAGCTGCTG ACTGGAGACG GTGCACGTCT GGACACGGGA GCACTTCCAC 120
253 TATGGGACTG GATACAGACA CACGCCCGGC GGA CTTC AAG ACAC TCA GAC TGAGGAGAAA 180
254 GCCCTGCCTG CTGCTGCTGC TGCTGCTGCT GCCACCGCTG CCTCTGAAGA CCCACTCCTT 240
255 TCATGGTTTT TCCTGCCAAG CCAGAGGCAC CTTCGCTGCT ACGGCCTTTC TCTGTGGTGT 300
256 CATTCAGCGG CTGGCCAGAG G ATG AGA CTC CCC AAA CTC CTC ACT CTT TTG 351
257 Met Arg Leu Pro Lys Leu Leu Thr Leu Leu
258 1 5 10
260 CTG TGG CAC CTG GCT TGG CTG GAC CTG GAA CTC ATC TGC ACT GTG CTG 399
261 Leu Trp His Leu Ala Trp Leu Asp Leu Glu Leu Ile Cys Thr Val Leu
262 15 20 25
264 GGT GCC CCT GAC TTA GGA CAG AGA ACC CCA GGG GCC AAG CCA GGG TTG 447
265 Gly Ala Pro Asp Leu Gly Gln Arg Thr Pro Gly Ala Lys Pro Gly Leu
266 30 35 40
268 ACC AAA GCG GAG GCC AAG GAG AGG CCA CCC CTG GCC AGG AAT GTC TTT 495
269 Thr Lys Ala Glu Ala Lys Glu Arg Pro Pro Leu Ala Arg Asn Val Phe
270 45 50 55
272 AGG CCA GGG GGT CAT ATC TAT GGT GTG GGG GCC ACC AAT GCC AGG GCC 543
273 Arg Pro Gly Gly His Ile Tyr Gly Val Gly Ala Thr Asn Ala Arg Ala
274 60 65 70
276 AAG GGA AGC TCT GGG CAG ACA CAG GCC AAG AAG GAT GAA CCC AGA AAG 591
277 Lys Gly Ser Ser Gly Gln Thr Gln Ala Lys Lys Asp Glu Pro Arg Lys
278 75 80 85 90
280 ATG CCC CCC AGA TCC GGT GGC TCT GAA ACC AAG CCA GGA CCC TCT TCC 639
281 Met Pro Pro Arg Ser Gly Gly Ser Glu Thr Lys Pro Gly Pro Ser Ser
282 95 100 105
284 CAG ACT AGA CAG GCT GCA GCC CGG ACT GTA ACC CCA AAA GGA CAG CTT 687
285 Gln Thr Arg Gln Ala Ala Ala Arg Thr Val Thr Pro Lys Gly Gln Leu
286 110 115 120
288 CCT GGG GGC AAA GCA TCT TCA AAA GCA GGA TCT GCC CCC AGC TCC TTC 735
289 Pro Gly Gly Lys Ala Ser Ser Lys Ala Gly Ser Ala Pro Ser Ser Phe

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## VERIFICATION SUMMARY

DATE: 07/30/2001

PATENT APPLICATION: US/09/880,708

TIME: 12:12:04

Input Set : N:\Crf3\RULE60\09880708.txt

Output Set: N:\CRF3\07302001\I880708.raw

L:6 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]  
L:11 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:86 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]  
L:107 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]  
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:150 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]  
L:173 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]  
L:195 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]  
L:203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:221 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]  
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8